

STIC-Biotech/ChemLib

68880

Fr m: Scheiner, Laurie
Sent: Friday, June 14, 2002 10:56 PM
To: STIC-Biotech/ChemLib
Subject: seq. search request (09/808,212)

Please search SEQ ID NO:1 of application S.N. 09/808,212. Thanks!

Laurie Scheiner
Art Unit 1648
CM1 8E05
308-1122
8E12

RECEIVED
JUN 17 2002
STIC

if Contact:
Sheppard

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 6/21/02
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST(where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

GenCore version 4.5
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OM nucleic - nucleic search, using sw model.

Run on: June 19, 2002, 16:25:56 ; Search time 1700.19 Seconds
(Without alignments)
1976.686 Million cell updates/sec

Title: US-09-808-212a-1
Perfect score: 249
Sequence: 1 atgaacatlaattgctgctg.....ttaaattgctggaataa 249

Scoring table: IDENTITY_NTC
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estbda:*
2: em_estlum:*
3: em_estlin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	24.9	602	12	AZ372526 1M0124L21
2	58.6	23.5	518	10	AZ771492 1M0573L10
3	58.2	23.4	318	10	BM159325 EST561848
4	57.6	23.1	475	10	BM029212 IPSK10005
5	57.4	23.1	691	12	BH040136 RPCI-24-2
6	57.2	23.0	443	10	BM374465 EBP103_SO
7	57	22.9	379	10	BM164323 EST566846
8	57	22.9	380	10	BM162473 EST566996
9	57	22.9	359	10	BM165811 EST568334
10	57	22.9	608	10	BM165552 EST566075
11	55.8	22.4	715	10	BM170799 EST573322
12	55	22.1	550	10	BH264512 CH230-121
13	54.4	21.8	546	12	AZ600777 1M0418D18
14	54.4	21.8	596	12	AZ460541 1M0265124
15	54.2	21.8	481	10	BM441017 Ebed02_SQ
16	53.8	21.6	571	12	AO919110 RPCI-23-2
17	53.6	21.5	938	12	AZ676392 ENT4747TR

18	53.4	21.4	540	12	AZ813205
19	53.4	21.4	868	12	BH161951
20	53.2	21.4	725	12	BH180166
21	53	21.3	699	12	CNS03C21
22	53	21.3	718	12	CNS04PAC
23	53	21.3	878	12	AZ673988
24	53	21.3	970	12	BH137975
25	52.6	21.1	498	9	BE223146
26	52.6	21.1	976	12	AG136173
27	52.4	21.0	650	12	AZ722144
28	52.4	21.0	935	10	BE897269
29	51.8	20.8	421	12	AZ113646
30	51.8	20.8	865	12	AZ668061
31	51.8	20.8	917	12	BH148214
32	51.8	20.8	929	12	AZ688789
33	51.8	20.8	956	12	AZ167142
34	51.6	20.7	437	9	BE030214
35	51.6	20.7	476	10	BE579798
36	51.6	20.7	563	12	AZ026892
37	51.4	20.6	485	10	BM161844
38	51.4	20.6	861	12	AZ137643
39	51.2	20.6	382	12	BH043453
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41	51	20.5	326	9	BE223521
42	51	20.5	327	10	BE580799
43	51	20.5	330	10	BE580447
44	51	20.5	331	10	BG225320
45	51	20.5	333	10	BG224555

ALIGNMENTS

RESULT 1
AZ372526 602 bp DNA linear GSS 02-OCT-2000
LOCUS 1M0124L21F Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION clone UUC1M0124L21 F, DNA sequence.

ACCESSION AZ372526.1 GI:10486226

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 602

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUC1M0124L21"

/clone_lib="Mouse 10kb plasmid UUC1M library"

location/Qualifiers

1. 602

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUC1M0124L21"

/clone_lib="Mouse 10kb plasmid UUC1M library"

location/Qualifiers

1. 602

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUC1M0124L21"

/clone_lib="Mouse 10kb plasmid UUC1M library"

location/Qualifiers

1. 602

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUC1M0124L21"

/clone_lib="Mouse 10kb plasmid UUC1M library"

location/Qualifiers

1. 602

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUC1M0124L21"

/clone_lib="Mouse 10kb plasmid UUC1M library"

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA.
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0573 row: L column: 10
Seq primer: CACACAGGAACACACTGTGACC
Class: plasmid ends
High quality sequence stop: 518.
Location/Qualifiers
I. 518

	Query Match	24.9%	Score 62;	DB: 12;	Length 602;
	Best Local Similarity	53.3%	Pred. No. 0.11;		
	Matches 131;	Conservative	0;	Mismatches 115;	Indels 0;
	Gaps	0;			
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Db	180 AAGAGAAAGAACACAGAACACACAGAACACAGAACACAGAACACAGAACGCA	239			
OY	61 gttacatcaaattracttaattcttcagatggaaaagatalaacacagcagaatticaa	120			
Db	240 GCAGCGCAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGAA	299			
OY	121 ggacaccttgaagaagcaacagcagaagtcttacagatatgagactatttagcagaaga	180			
Db	300 GAAGAGAAGGA	359			

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (911473211419b1AR129072.1), a copy-number inducible derivative of plasmid r1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Accession	Definition	LOCUS	Result	Db	Oy	Db	Oy
A2771492	1M0573J10R Mouse 10kb plasmid U06C1M library Mus musculus genomic clone U06C1M0573J10 R, DNA sequence.	A2771492	2	420	241	420	241
A2771492		A2771492		GAGACA	gaaaaa	GAGACA	gaaaaa
A2771492		A2771492					
A2771492		A2771492					
A2771492.1		A2771492.1					
GI:12893811		GI:12893811					
GSS.		GSS.					
human mouse.		human mouse.					
Mus musculus		Mus musculus					

ORGANISM	REFERENCE	AUTHORS
<i>Mus musculus</i>		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus		
1 (pases 1 to 518)		
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, R., Hamil, C.		

TITLE Mouse whole genome scaffolding with paired end reads from 10Kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

[illegible]

RESULT	3
BMI59325	
LOCUS	BMI59325
DEFINITION	BMI59325 318 bp mRNA
ACCESSION	EST561848 PYBS Plasmodium yoelii cDNA clone pYCUC65 end,
VERSION	BMI59325
KEYWORDS	BMI59325.1 GI:17305009
SOURCE	EST.
ORGANISM	Plasmodium yoelii yoelii. Plasmodium yoelii yoelii.

REFERENCE 1 (bases 1 to 559)
AUTHORS Carlton J.M., Daly T.M., Long C.A., Bergman L.W., Valdy A.B.,
Fraser C.M. and Carucci D.J.
TITLE Plasmodium yoelli EST project at TIGR
JOURNAL Unpublished (2001)
COMMENT Contact: Jane Carlton
Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-9319
Fax: 301-838-0208
Email: carlton@tigr.org
For clone info, please contact the Malaria Research and Reference
Reagent Resource Center, ATCC
http://www.malaria.mr4.org/mr4pages/index.html
Seq primer: ADF.

FEATURES
source
1. 559
Location/Qualifiers
/organism="Plasmodium yoelli yoelli"
/strain="17XL"
/db_xref="taxon:73239"
/clone="PYCMT47"
/clone_1ib="PyBS"
/dev_stage="Asexual blood stages"
/lab_host="E. coli XL-1 Blue"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was
collected from BALB/CByJ mice infected with Py17XL
parasites, and leukocytes removed by passage over
microcrystalline cellulose columns. Total RNA was
isolated using the guanidium isothiocyanate method, and
mRNA isolated using oligo(dt)-cellulose chromatography.
First strand cDNA synthesis was completed using a 50-base
primer and reverse transcriptase in the presence of
5-methyl dCTP. After second strand synthesis, uneven
termini were treated with Pfu DNA polymerase and EcoRI
adaptors ligated to the blunt ends. The sample was cleaved
with XhoI and separated on a Sephacryl S-500 column.
Size-fractionated cDNA was precipitated and ligated to
HybridZAP arms directionally using EcoRI-XhoI cleaved arms.
After packaging, the phagemid vector (pAD-GAL4) was
excised from the HybridZAP vector and plasmid DNA
isolated."

BASE COUNT 285 a 58 c 117 g 99 t
ORIGIN

Query Match 22.9%; Score 57; DB 10; Length 559;
Best Local Similarity 55.2%; Pred. No. 0.77;
Matches 111; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

Oy 5 acattaatttctgtaaaagaaacacacagaaacacacagaaagaaagaaagaa 64
Db 253 AAACAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 312
Oy 65 caataaagtttaacttaactcttgcagatgtaaaagatacaacaacagaaattcaagaa 124
Db 313 AAGAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 372
Oy 125 cattgaagaagcaacagcagacagattacagatatgcagactattagcaaaagtaatg 184
Db 373 CAAAAGAAAGCTGCAGAGAAAGCTGCAAAAGAAAGCTGCAAAAGAAAGCTG 432
Oy 185 gcaatatatacagcagactag 205
Db 433 CAGAGAAAGCTGCAGAAATGAAG 453

RESULT 10
BM163552 608 bp mRNA linear EST 04-DEC-2001
LOCUS BM163552
DEFINITION EST566075 PyBS Plasmodium yoelli yoelli cDNA clone pYCLG59 5' end,
mRNA sequence.

ACCESSION BM163552
VERSION BM163552.1 GI:17309233
KEYWORDS EST
SOURCE Plasmodium yoelli yoelli.
ORGANISM Plasmodium yoelli yoelli.
REFERENCE 1 (bases 1 to 608)
AUTHORS Carlton J.M., Daly T.M., Long C.A., Bergman L.W., Valdy A.B.,
Fraser C.M. and Carucci D.J.
TITLE Plasmodium yoelli EST project at TIGR
JOURNAL Unpublished (2001)
COMMENT Contact: Jane Carlton
Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-9319
Fax: 301-838-0208
Email: carlton@tigr.org
For clone info, please contact the Malaria Research and Reference
Reagent Resource Center, ATCC
http://www.malaria.mr4.org/mr4pages/index.html
Seq primer: ADF.

FEATURES
source
1. 608
Location/Qualifiers
/organism="Plasmodium yoelli yoelli"
/strain="17XL"
/db_xref="taxon:73239"
/clone="PYCLG59"
/clone_1ib="PyBS"
/dev_stage="Asexual blood stages"
/lab_host="E. coli XL-1 Blue"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was
collected from BALB/CByJ mice infected with Py17XL
parasites, and leukocytes removed by passage over
microcrystalline cellulose columns. Total RNA was
isolated using the guanidium isothiocyanate method, and
mRNA isolated using oligo(dt)-cellulose chromatography.
First strand cDNA synthesis was completed using a 50-base
primer and reverse transcriptase in the presence of
5-methyl dCTP. After second strand synthesis, uneven
termini were treated with Pfu DNA polymerase and EcoRI
adaptors ligated to the blunt ends. The sample was cleaved
with XhoI and separated on a Sephacryl S-500 column.
Size-fractionated cDNA was precipitated and ligated to
HybridZAP arms directionally using EcoRI-XhoI cleaved arms.
After packaging, the phagemid vector (pAD-GAL4) was
excised from the HybridZAP vector and plasmid DNA
isolated."

BASE COUNT 304 a 61 c 111 g 132 t
ORIGIN

Query Match 22.9%; Score 57; DB 10; Length 608;
Best Local Similarity 55.2%; Pred. No. 0.76;
Matches 111; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

Oy 5 acattaatttctgtaaaagaaacacacagaaacacacagaaagaaagaaagaa 64
Db 59 AAACAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 118
Oy 65 caataaagtttaacttaactcttgcagatgtaaaagatacaacaacagcagaaattcaagaa 124
Db 119 AAGAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 178
Oy 125 cattgaagaagcaacagcagacagattacagatatgcagactattagcaaaagtaatg 184
Db 179 CAAAAGAAAGCTGCAGAGAAAGCTGCAAAAGAAAGCTGCAAAAGAAAGCTG 238
Oy 185 gcaatatatacagcagactag 205
Db 239 CAGAGAAAGCTGCAGAAATGAAG 259

Query Match	21.8%	Score	54.4	DB	12	Length	546
Best Local Similarity	53.2%	Pred. No	2.2				
Matches	115	Conservative	0	Mismatches	101	Indels	0
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M026512A"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-".
/notes="Vector: pWD42mv; Purified genomic DNA from Mus musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The ligated DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g1147321149b) (AF129072.1), a copy number

```


GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 17:34:34 ; Search time 46.05 Seconds
(without alignments)
1328.181 Million cell updates/sec

Title: US-09-808-212a-1
Perfect score: 249
Sequence: 1 atgaacatcaattgtctg.....ttaaattgtgaaataa 249

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues
Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/1/ina/PTOUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfill1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	DB ID	Description
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2	229.8	92.3	3279 4 US-08-446-137B-1	Sequence 1, Appli
3	181.2	72.8	921 2 US-08-795-475-2	Sequence 2, Appli
4	181.2	72.8	1308 2 US-08-795-475-4	Sequence 4, Appli
5	109.8	44.1	548 3 US-08-828-741B-1	Sequence 1, Appli
6	109.8	44.1	548 4 US-09-160-567-1	Sequence 1, Appli
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9	107	43.0	599 3 US-08-828-741B-7	Sequence 7, Appli
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23	44	17.7	1482 4 US-08-462-625-41	Sequence 41, Appli
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27	42.8	17.2	696 4 US-09-461-697-193	Sequence 193, App

28	42.8	17.2	699 4 US-09-461-697-191	Sequence 191, App
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30	42.8	17.2	774 4 US-09-461-697-187	Sequence 187, App
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32	42.8	17.2	1669 4 US-09-461-697-184	Sequence 184, App
33	42	16.9	864 4 US-08-858-207A-132	Sequence 132, App
34	41	16.5	289 4 US-09-007-005-17	Sequence 17, Appli
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36	41	16.5	397 3 US-09-253-691-3	Sequence 3, Appli
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42	40.2	16.1	213 4 US-09-461-697-209	Sequence 209, App
43	40	16.1	240 1 US-08-628-417-6	Sequence 6, Appli
44	39.8	16.0	1276 1 US-09-177-325-2	Sequence 2, Appli
45	39.8	16.0	1276 4 US-09-411-812A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-446-137B-3
Sequence 3, Application US/08446137B
Patent No. 6162903
GENERAL INFORMATION:
APPLICANT: Trower, Angus R.
APPLICANT: Atkinson, Anthony
APPLICANT: Murphy, Jonathan P.
APPLICANT: Laurence, Oliver S.
APPLICANT: Dugleby, Clive J.
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEINS DERIVED FROM L PROTEIN AND THEIR USES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,137B
FILING DATE: 22-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 100084,406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 876 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: *Peptostreptococcus*
STRAIN: 1018
FEATURE:

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SEQUENCE CHARACTERISTICS:
LENGTH: 3279 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

```

CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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?      ZIP: 11530
?
?      COMPUTER READABLE FORM:
?
?      MEDIUM TYPE: Floppy disk
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?      COMPUTER: IBM PC compatible
?
?      OPERATING SYSTEM: PC-DOS/MS-DOS
?
?      SOFTWARE: PatentIn Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,741B
FILING DATE: 26-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 548 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..548
US-08-828-741B-1

Query Match 44.1%; Score 109.8; DB 3; Length 548;
Best Local Similarity 68.0%; Pred. No. 2.5e-18;
Matches 153; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
DB 25 gaacaccagaacaccagagagacacaaagaagattacatacaagttacttaac 84
52 GTAGCGAGGCGCCCTCGAAGATACACGAGAGAGTACGATCAAGGAGCACTGATC 111
QY 85 ttgcagatggaagaatatacaacagcagaatttaagaagacatttaagaagaacagca 144
DB 112 TTTCGAATGTGACACACAACTGCAAGATTAAGGTACTTCGAAAAGCGACTCG 171
QY 145 gaagcttaagaatagcagacttattagcaaaagtaaatgycgaatatatacagcagctta 204
DB 172 GAAGCTTATGCGTATGACATCTTGTGAAGAAAGACAAATGCTGAATATCTGATATGTT 231
QY 205 gaagatggtggaacacatatgaacataatttgcgtggaataaa 249
DB 232 GCAGATTAAGGTTACACCTGAAACATCAAAATTCGCGGTAAGAA 276

RESULT 6
US-09-160-567-1
Sequence 1, Application US/09160567
Patent No. 6326179
GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
City: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,567
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,741
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 548 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..548
US-09-160-567-1

Query Match 44.1%; Score 109.8; DB 4; Length 548;
Best Local Similarity 68.0%; Pred. No. 2.5e-18;
Matches 153; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
DB 25 gaacaccagaacaccgagagacacaaagaagattacatacaagttacttaac 84
52 GTAGCGAGGCGCCCTCGAAGATTAACACGAGAGAGTACGATCAAGGAGCACTGATC 111
QY 85 ttgcagatggaagaatatacaacagcagaatttaagaagacatttgaagaagaacagca 144
DB 112 TTTCGAATGTGACACACAACTGCAAGATTAAGGTACTTCGAAAAGCGACTCG 171
QY 145 gaagcttaagaatagcagacttattagcaaaagtaaatgycgaatatatacagcagctta 204
DB 172 GAAGCTTATGCGTATGACATCTTGTGAAGAAAGACAAATGCTGAATATCTGATATGTT 231
QY 205 gaagatggtggaacacatatgaacataatttgcgtggaataaa 249
DB 232 GCAGATTAAGGTTACACCTGAAACATCAAAATTCGCGGTAAGAA 276

RESULT 7
US-08-828-741B-12
Sequence 12, Application US/08828741B
Patent No. 6043069
GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
City: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,741B
FILING DATE: 26-MAR-1997

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 539 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..539
US-08-828-741B-12

Query Match 43.08; Score 107; DB 3; Length 539;
Best Local Similarity 71.88; Pred. No. 1.2e-17;
Matches 140; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 55 gaagaatttaacatcaagaatttaacttaacttccttcagatggaagaagatcacacagacagaa 114
DB 34 GAAGAAGTCACGATCAAAAGCAGACCTGATCTTTCGAATGTGTACACACAAACTGCAGAA 93
QY 115 ttcaagaagaacttgaagaagaacagcagagacttacagatatgcagacttattgca 174
DB 94 TTCAAGGACTCTCGAAAAAGCGACCTCGAGAGCTTATGCGTATGCGATGATCTTGAAG 153
QY 175 aaagtaaatgycgatatacatagcagacttagaagatgltggaaccatatagaacattaa 234
DB 154 AAAGCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 213
QY 235 ttctctgaaataa 249
DB 214 TTCCGGGGTAAGAA 228

RESULT 8
US-09-160-567-12
Sequence 12, Application US/09160567
Patent No. 6326179
GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,567
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,741

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 539 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..539
US-09-160-567-12

Query Match 43.08; Score 107; DB 4; Length 539;
Best Local Similarity 71.88; Pred. No. 1.2e-17;
Matches 140; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 55 gaagaatttaacatcaagaatttaacttaacttccttcagatggaagaagatcacacagacagaa 114
DB 34 GAAGAAGTCACGATCAAAAGCAGACCTGATCTTTCGAATGTGTACACACAAACTGCAGAA 93
QY 115 ttcaagaagaacttgaagaagaacagcagagacttacagatatgcagacttattgca 174
DB 94 TTCAAGGACTCTCGAAAAAGCGACCTCGAGAGCTTATGCGTATGCGATGATCTTGAAG 153
QY 175 aaagtaaatgycgatatacatagcagacttagaagatgltggaaccatatagaacattaa 234
DB 154 AAAGCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 213
QY 235 ttctctgaaataa 249
DB 214 TTCCGGGGTAAGAA 228

RESULT 9
US-08-828-741B-7
Sequence 7, Application US/08828741B
Patent No. 6043069
GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,741B
FILING DATE: 26-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.

RESULT 10
 US-09-160-567-J
 Sequence 7, Application US/09160567
 Patent No. 6326179
 GENERAL INFORMATION:
 APPLICANT: Koentgen, Frank
 APPLICANT: Suess, Gabriele M.
 APPLICANT: Tarlinton, David M.
 APPLICANT: Treutlein, Herbert R.
 TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
 TITLE OF INVENTION: PRODUCING SAME
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: New York
 COUNTRY: United States of America
 ZIP: 11530
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/160,567
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/828,741
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Digiglio, Frank S.

RESULT 11
US-08-828-741B-5
Sequence 5 Application US/08828741B
Patent No. 6043069
GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SCULLY, MURPHY & PRESSER
STREET: 400 Garden City Plaza
City: Garden City
STATE: New York
COUNTRY: United States of America
Zip: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,741B
FILING DATE: 26-Mar-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DigiGlio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1031 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1031
US-08-828-741B-5

Query Match 43.0%; Score 107; DB 3; Length 1031;
Best Local Similarity 66.0%; Pred. No. 1.3e-17;
Matches 155; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 15 tgcctggaagaagacacacagagaacacagagaacacagagaagttacatcaaat 74
DB 486 TGGTGTGTCGCAAAACCTGCTTCTCCAGGTGTGAGCCCGAAGAGTCACGATCAAAAGC 545
QY 75 taacttaattcttgcaagatggaagatacaaacagcagaattcaaaaggaacattggaaga 134
DB 546 GAACCTGATCTTTGCAATGTGTAGACACACAACATGCAAGTCAAGTACTTGCAAAA 605
QY 135 agcaacagcagaagcttcagatatgcagacttattagcaaaagtaaatgacgaatatac 194
DB 606 AGCAGCCCTCGGAGAGCTTATGCGTATGCAATCTTTGAAGAAAGCAATGCTGATATAC 665
QY 195 agcagacttaagaatggtggaagacataatgaacattaaatttctggaataata 249
DB 666 TGTGATGTTCAGATTAAGGTTACACCTGACATCAATTCGGGGTAAGAA 720

RESULT 12

US-09-160-567-5
Sequence 5, Application US/09160567
Patent No. 6326179

GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Sues, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
NUMBER OF INVENTIONS: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,567
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,741
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1031 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1031
US-09-160-567-5

Query Match 43.0%; Score 107; DB 4; Length 1031;
Best Local Similarity 66.0%; Pred. No. 1.3e-17;
Matches 155; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 15 tgcctggaagaagacacacagagaacacagagaacacagagaagttacatcaaat 74
DB 486 TGGTGTGTCGCAAAACCTGCTTCTCCAGGTGTGAGCCCGAAGAGTCACGATCAAAAGC 545
QY 75 taacttaattcttgcaagatggaagatacaaacagcagaattcaaaaggaacattggaaga 134
DB 546 GAACCTGATCTTTGCAATGTGTAGACACACAACATGCAAGTCAAGTACTTGCAAAA 605
QY 135 agcaacagcagaagcttcagatatgcagacttattagcaaaagtaaatgacgaatatac 194
DB 606 AGCAGCCCTCGGAGAGCTTATGCGTATGCAATCTTTGAAGAAAGCAATGCTGATATAC 665
QY 195 agcagacttaagaatggtggaagacataatgaacattaaatttctggaataata 249
DB 666 TGTGATGTTCAGATTAAGGTTACACCTGACATCAATTCGGGGTAAGAA 720

RESULT 13

US-08-828-741B-3
Sequence 3, Application US/08828741B
Patent No. 6043069

GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Sues, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
NUMBER OF INVENTIONS: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,741B
FILING DATE: 26-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1490 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1490

US-08-828-741B-3

Query Match 43.0%; Score 107; DB 3; Length 1490;

Best Local Similarity 66.0%; Pred. No. 1.4e-17;

Matches 155; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

OY 15 tgcctggaagaagaacacacagaaacacagaaagaaacaaagaagattacatcaagt 74

DB 486 TGGTGTAGCGAAGAAACCTGACTTCAGGGTGTAGCGCGGAGAGATCAGATCAAGC 545

OY 75 taacttaattcttgcagatgaaagatatacaacagcagagattcaaggaatttgaaga 134

DB 546 GAACCTGATCTTGCAGAAAGTGACACACAACTCGAGATTCAGATTCAGTTCGAAA 605

OY 135 agcaacagcagaagcttacagatatgcagacttattagcaaaagttaattgagatatac 194

DB 606 AGCGACCTCGAGAGCTTATCGTATGACAGATCTTGAAGAAAGACAAATGGTGAATATAC 665

OY 195 agcagacttaagatggttgaaacatataagacatttaatttgcgtgaataata 249

DB 666 TGTAGATGTGCAGATTAAGGTTACACCTGACATCAATTCGCGGTAAGAA 720

RESULT 14

US-09-160-567-3

Sequence 3, Application US/09160567,

Patent No. 6326179

GENERAL INFORMATION:

APPLICANT: Koentgen, Frank

APPLICANT: Suess, Gabriele M.

APPLICANT: Tarlington, David M.

APPLICANT: Treutlein, Herbert R.

TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF

TITLE OF INVENTION: PRODUCING SAME

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: United States of America

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/160,567

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/828,741

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: DIGILIO, Frank S.

REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 10591

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1490 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1490

US-09-160-567-3

Query Match 43.0%; Score 107; DB 4; Length 1490;

Best Local Similarity 66.0%; Pred. No. 1.4e-17;

Matches 155; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

OY 15 tgcctggaagaagaacacacagaaacacagaaagaaacaaagaagattacatcaagt 74

DB 486 TGGTGTAGCGAAGAAACCTGACTTCAGGGTGTAGCGCGGAGAGATCAGATCAAGC 545

OY 75 taacttaattcttgcagatgaaagatatacaacagcagagattcaaggaatttgaaga 134

DB 546 GAACCTGATCTTGCAGAAAGTGACACACAACTCGAGATTCAGATTCAGTTCGAAA 605

OY 135 agcaacagcagaagcttacagatatgcagacttattagcaaaagttaattgagatatac 194

DB 606 AGCGACCTCGAGAGCTTATCGTATGACAGATCTTGAAGAAAGACAAATGGTGAATATAC 665

OY 195 agcagacttaagatggttgaaacatataagacatttaatttgcgtgaataata 249

DB 666 TGTAGATGTGCAGATTAAGGTTACACCTGACATCAATTCGCGGTAAGAA 720

RESULT 15

US-08-072-610-1

Sequence 1, Application US/08072610

Patent No. 5532133

GENERAL INFORMATION:

APPLICANT: Barnwell, John

TITLE OF INVENTION: Plasmodium vivax blood stage Antigens,

TITLE OF INVENTION: Monoclonal Antibodies, and Diagnostic Assays

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Darby and Darby

STREET: 805 Third Ave.

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10022-7513

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/072,610

FILING DATE: 19930602

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: GOGORIS, Adda

REGISTRATION NUMBER: 29,714

REFERENCE/DOCKET NUMBER: 5986/07686

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)527-7700

TELEFAX: (212)753-6237

TELEX: 236687

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 337 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Plasmodium vivax
IMMEDIATE SOURCE:
CLONE: PVMB3.3.1
US-08-072-610-1

Query Match 20.3%; Score 50.6; DB 1; Length 3337;
Best Local Similarity 53.9%; Pred. No. 0.00061;
Matches 104; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

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Db	1278	GGAGAAGTATCAGAGAACTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT	1337
Oy	79	ttaactttgcagatggaagatacaaacagcagaattcaagaagacattgaagaagca	138
Db	1338	GATTTCGATTAGATGAGACTACATTAGAGAAACCGAAGAACTCGAGAGAGAGAGAA	1397
Oy	139	acagcagaagcttacagatatgcagaacttattagcaaaagtaaatgycgaatatacagca	198
Db	1398	ACCGTAGAGGAGAGAAACCGTAGAGGAGAGAGAAACCGTAGAGGAGAGAAAGCTGCA	1457
Oy	199	gacttagaagatg	211
Db	1458	GAAGGAGAGAGAG	1470

Search completed: June 19, 2002, 18:43:44
Job time: 4150 sec

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 17:38:59 ; Search time 214.27 Seconds
(without alignments)
1995.201 Million cell updates/sec

Title: US-09-808-212a-1
Perfect score: 249
Sequence: 1 atgaacattaaattgtctgtg.....ttaattgtctggaataaa 249

Scoring table:
IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 segs, 858457221 residues
Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	249	100.0	249	21	AAA08425
2	245.8	98.7	249	21	AAA08443
3	244.2	98.1	249	21	AAA08442
4	244.2	98.1	249	21	AAA08445
5	241	96.8	249	21	AAA08444
6	231.4	92.9	876	14	AA050947
7	229.8	92.3	3279	14	AA050946
8	229.8	92.3	3279	14	AA051536
9	209	83.9	225	21	AAA08433

10	204.4	82.1	222	21	AAA08432	Peptostreptococcus
11	191.8	77.0	213	21	AAA08431	Peptostreptococcus
12	181.2	72.8	921	14	AA050452	Sequence encoding
13	181.2	72.8	1305	22	AA084644	Profilin-GDPex encod
14	181.2	72.8	1305	22	AA084644	Nucleotide sequenc
15	181.2	72.8	1308	14	AA050453	Sequence encoding
16	181.2	72.8	1418	22	AA084644	Nucleotide sequenc
17	171.8	69.0	216	21	AAA08429	Peptostreptococcus
18	166.4	66.8	216	21	AAA08428	Peptostreptococcus
19	156.8	63.0	216	21	AAA08427	Peptostreptococcus
20	136.4	54.8	228	21	AAA08426	Peptostreptococcus
21	127.2	51.1	213	21	AAA08430	Peptostreptococcus
22	109.8	44.1	548	20	AA084590	Growth factor LHL
23	109.8	44.1	539	18	AA084591	DNA encoding a LHL
24	107	43.0	539	18	AA084591	Growth factor LHL
25	107	43.0	539	18	AA084591	DNA encoding a for
26	107	43.0	539	18	AA084591	Growth factor LHL
27	107	43.0	539	18	AA084591	DNA encoding a for
28	107	43.0	1031	18	AA084591	DNA encoding a for
29	107	43.0	1031	20	AA084592	Growth factor TLHL
30	107	43.0	1479	20	AA084596	DNA encoding a ccm
31	107	43.0	1490	18	AA084587	Growth factor CATB
32	107	43.0	1490	20	AA084591	DNA encoding CATB
33	86.2	34.6	6094	21	AA084587	Expression vector
34	58.6	23.5	1686	16	AA084587	DNA encoding Leuco
35	56	22.5	379	23	AA084587	DNA encoding novel
36	56	22.5	379	23	AA084587	DNA encoding novel
37	56	22.5	3399	17	AA084586	Chicken leucocytes
38	56	22.5	3399	17	AA084586	Plasmodium falcipar
39	53.2	21.4	1407	21	AA084587	DNA encoding novel
40	52.8	21.2	29392	19	AA084587	Mouse poly Ig rece
41	51.4	20.6	483	23	AA084587	DNA encoding novel
42	51.2	20.6	1167	23	AA084587	DNA encoding novel
43	50.6	20.3	3337	17	AA084587	P. vivax ESP-1 blo
44	50.6	20.3	3337	20	AA084587	DNA encoding a sec
45	50.6	20.3	3337	22	AA084587	Plasmodium vivax E

ALIGNMENTS

RESULT 1	
AAA08425	AAA08425 standard; DNA: 249 BP.
XX	20-JUL-2000 (first entry)
AC	20-JUL-2000 (first entry)
XX	
DT	
DE	Ig Light chain binding protein P/L construct DNA sequence SPQ ID NO:1.
XX	
KW	Immunoglobulin light chain binding protein; P/L; protein L;
KW	Peptostreptococcus; human immunoglobulin kappa chain;
KW	Immunofluorescence chromatography; ds.
XX	
OS	Peptostreptococcus sp.
XX	
PM	WO200015803-A1.
XX	
PD	23-MAR-2000.
XX	
PF	14-SEP-1999; 99WO-GB03048.
XX	
PR	14-SEP-1998; 98GB-0019998.
XX	
PA	26-APR-1999; 99GB-0009578.
XX	
PI	(ACTI-) ACTINOVA LTD.
XX	
PI	Gore MG, Beckingham JA, Roberts SE;
XX	
DR	WPI: 2000-271441/23.
XX	
DR	P-PSDB: AAY82536.
XX	

DR WFL, 2000 2/11/11
DR P-PSDB; AAY82546

DR. WEL, 2000 214747-23

DR P-PSDB; AAY82545.
XX New modified immunoglobulin light chain binding protein, useful in
PT immunofinity chromatography, has a dissociation constant of 400 nM or
PT more at pH8 with respect to human immunoglobulin kappa-chain -
XX
XX Example 1; Page 50-51; 56pp; English.
PS
XX The present invention describes an immunoglobulin (Ig) light chain
CC binding protein (PI) which has been modified by one or more amino acid
CC substitutions such that the dissociation constant (Kd) of the protein
CC with respect to human Ig kappa-chain is 400 nM or more at pH8. PI is
CC useful in immunofinity chromatography. The present sequence encodes a
CC mutant Peptostreptococcus protein L, which is an Ig light chain binding
CC protein, from the present invention.
XX
SQ Sequence 249 BP; 117 A; 36 C; 47 G; 49 T; 0 other;

Query Match 98.1%; Score 244.2; DB 21; Length 249;
Best Local Similarity 98.8%; Pred. No. 6.5e-44;
Matches 246; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 atgaacattaaatttcttggaagaacaccagaaacacccagagaagaaacaaagaaga 60
Db 1 atgaacattaaatttcttggaagaacaccagaaacacccagagaagaaacaaagaaga 60
QY 61 gttaacatcaaatgtaacttaattcttgagatggaagatacaaacagcagaattcaaa 120
Db 61 gttaacatcaaatgtaacttaattcttgagatggaagatacaaacagcagaattcaaa 120
QY 121 ggaacatttgaagaagacagcagaagcttacagatatgagacttattgacaaagta 180
Db 121 ggaacatttgaagaagacagcagaagcttacagatatgagacttattgacaaagta 180
QY 181 aatggcgaatatatacagcagacttagaagatggtggaacccatatacattaaatttgc 240
Db 181 aatggcgaatatatacagcagacttagaagatggtggaacccatatacattaaatttgc 240
QY 241 ggaataataa 249
Db 241 ggaataataa 249

RESULT 4

AAA08445
ID AAA08445 standard; DNA: 249 BP.

AC AAA08445;

DT 20-JUL-2000 (first entry)

DE PPL mutant nucleotide sequence SEQ ID NO:22.

XX Immunoglobulin light chain binding protein; PPL; protein L;
KW Peptostreptococcus; human immunoglobulin kappa chain; mutant;
KW immunofinity chromatography; site directed mutagenesis; ds.
XX
OS Peptostreptococcus sp.
XX
PN WO200015803-A1.
XX
PD 23-MAR-2000.
XX
PF 14-SEP-1999; 99WO-GB03048.
XX
PR 14-SEP-1998; 98GB-0019998.
PR 26-APR-1999; 99GB-0009578.
XX
PA (ACTI-) ACTINOVA LTD.
XX
PI Gore MG, Beckingham JA, Roberts SE;
XX

DR WPI; 2000-271441/23.
DR P-PSDB; AAY82548.

XX New modified immunoglobulin light chain binding protein, useful in
PT immunofinity chromatography, has a dissociation constant of 400 nM or
PT more at pH8 with respect to human immunoglobulin kappa-chain -
XX
XX Example 1; Page 53; 56pp; English.
PS
XX

CC The present invention describes an immunoglobulin (Ig) light chain
CC binding protein (PI) which has been modified by one or more amino acid
CC substitutions such that the dissociation constant (Kd) of the protein
CC with respect to human Ig kappa-chain is 400 nM or more at pH8. PI is
CC useful in immunofinity chromatography. The present sequence encodes a
CC mutant Peptostreptococcus protein L, which is an Ig light chain binding
CC protein, from the present invention.
XX
SQ Sequence 249 BP; 116 A; 37 C; 47 G; 49 T; 0 other;

Query Match 98.1%; Score 244.2; DB 21; Length 249;
Best Local Similarity 98.8%; Pred. No. 6.5e-44;
Matches 246; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 atgaacattaaatttcttggaagaacaccagaaacacccagagaagaaacaaagaaga 60
Db 1 atgaacattaaatttcttggaagaacaccagaaacacccagagaagaaacaaagaaga 60
QY 61 gttaacatcaaatgtaacttaattcttgagatggaagatacaaacagcagaattcaaa 120
Db 61 gttaacatcaaatgtaacttaattcttgagatggaagatacaaacagcagaattcaaa 120
QY 121 ggaacatttgaagaagacagcagaagcttacagatatgagacttattgacaaagta 180
Db 121 ggaacatttgaagaagacagcagaagcttacagatatgagacttattgacaaagta 180
QY 181 aatggcgaatatatacagcagacttagaagatggtggaacccatatacattaaatttgc 240
Db 181 aatggcgaatatatacagcagacttagaagatggtggaacccatatacattaaatttgc 240
QY 241 ggaataataa 249
Db 241 ggaataataa 249

RESULT 5

AAA08444
ID AAA08444 standard; DNA: 249 BP.

AC AAA08444;

DT 20-JUL-2000 (first entry)

DE PPL mutant nucleotide sequence SEQ ID NO:21.

XX Immunoglobulin light chain binding protein; PPL; protein L;
KW Peptostreptococcus; human immunoglobulin kappa chain; mutant;
KW immunofinity chromatography; site directed mutagenesis; ds.
XX
OS Peptostreptococcus sp.
XX
PN WO200015803-A1.
XX
PD 23-MAR-2000.
XX
PF 14-SEP-1999; 99WO-GB03048.
XX
PR 14-SEP-1998; 98GB-0019998.
PR 26-APR-1999; 99GB-0009578.
XX
PA (ACTI-) ACTINOVA LTD.
XX
PI Gore MG, Beckingham JA, Roberts SE;
XX

Field	Key	Location/Qualifiers
FT	repeat_unit	1..96
FT		/*tag=
FT		a
FT		"Repeat units are not adjacent, repetitions
FT		of this sequence are not 100% homologous and
FT		begin at nucleotide positions 214, 427 and
FT		649"
FT	repeat_unit	97..210
FT		/*tag=
FT		b
FT		/*note=
FT		"Repeat units are not adjacent, repetitions
FT		of this sequence are not 100% homologous and
FT		begin at nucleotide positions 313, 535 and

QY	1	atgacattaatcttgctggaagaagaaacaccagaacacacagagaagaccaaaagaagaa	60
Db	628	atcaacattaatcttgctggaagaagaacaccagaaacaccagaagaagccaaaagaagaa	687
QY	61	gttcaatcaaaagttaaccttaattcttgcagatggaagatgacaacagcagaattcaaa	120
Db	688	gttcaatcaaaagttaaccttaattcttgcagatggaagatgacaacagcagaattcaaa	747
QY	121	ggaacatttgaagaagcaacagcagcagaagcttacagatatcagaacttattagcaaaagta	180
Db	748	ggaacatttgaagaagcaacagcagcagaagcttacagatatcagaacttattagcaaaagta	807
QY	181	aatgagcaatatcagacagagcttagaagatggtggaacacatatgaaacattaaattgct	240
Db	808	aatgtagaatcagacagagcttagaagatggtgcgatatcactatcaacatcaaatctgct	867
QY	241	ggaataataa 249	
Db	868	ggaaataata 876	

RESULT	7
AAQ50946	
ID	AAQ50946 standard; cDNA; 3279 BP.
XX	
AC	AAQ50946;
XX	
DT	18-MAY-1994 (first entry)
XX	
DE	Sequence encoding protein L.
XX	
KW	Peptide; immunoglobulin; binding; analysis; purification; ELISA.
XX	enzyme linked immunosorbant assay; ss.
XX	

Query Match	Similarity	Score	DB	Length
Best Local Similarity	95.2%	229.8	14	3279
Matches	237	Conservative	0	Mismatches 12; Indels 0; Gaps 0;
1	atgaacattaaattgtctgtaaaagaacaccagaaacacacagaagaacccaagaaga	60		
1576	atcacattaaattgtctgtaaaagaacaccagaaacacacagaagaacccaagaaga	1635		
61	gttcaatcaaatgtaacttaattcttgcagaatgtgaaagatacacaacgcgaattcaa	120		
121	ggaacatttgaagagcacagcagaagaacttacagatatgcagacttatagcaaaagta	180		
1696	ggaacatttgaagagcacagcagaagaacttacagatatgcagacttatagcaaaagta	1755		
181	aatggcaatatcacagcagaacttgaagaatggtgaaacatatgaacattaattgtct	240		
1756	aatggttatacacagcagaacttgaagaatggtgatacattcaacataaattgtct	1815		
241	ggaataataa 249			
1816	ggaataataa 1824			
8	AA051556			
AA051556	standard; cDNA; 3279 BP.			
18-MAY-1994	(first entry)			
Sequence encoding protein L.				
Protein; immunoglobulin; binding; immobilisation; light chains;				
antibodies; diagnosis; pharmaceutical; ss.				
Peptococcus magnus.				
Location/Qualifiers				
103..3185				
/*tag= a				
/product= Protein L.				
490..573				
/*tag= b				
/note=	"Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide positions 673 and 856"			
574..672				
/*tag= c				
/note=	"Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide position 757"			
949..1044				
/*tag= d				
/note=	"Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide positions 1162, 1375 and 1597"			
1045..1158				
/*tag= e				
/note=	"Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide positions 1261, 1483 and 1705"			
1822..1938				
/*tag= f				
/note=	"Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide positions 2347 and 2545"			


```
RESULT 10
AAA08432
ID AAA08432 standard; DNA: 222 BP.
XX
XX
AC AAA08432;
XX
XX 20-JUL-2000 (first entry)
XX
XX Peptostreptococcus strain 3316 protein L domain C3 DNA sequence.
XX
XX
XX Immunoglobulin light chain binding protein; PpL; protein L;
XX Peptostreptococcus; human immunoglobulin kappa chain;
XX Immunofaffinity chromatography; ds.
XX
XX Peptostreptococcus sp.
XX WO200015803-A1.
XX
XX 23-MAR-2000.
XX
XX 14-SEP-1999; 99WO-GB03048.
XX
XX 14-SEP-1998; 98GB-0019998.
XX 26-APR-1999; 99GB-0009578.
XX
XX (ACTI-) ACTINOVA LTD.
XX
XX Gore MG, Beckingham JA, Roberts SE;
XX WPI: 2000-271441/23.
XX P-PSDB; AAY82543.
XX
XX New modified immunoglobulin light chain binding protein, useful in
XX immunofaffinity chromatography, has a dissociation constant of 400 nM or
XX more at pH8 with respect to human immunoglobulin kappa-chain -
XX
XX Disclosure; Page 48; 56pp; English.
XX
XX The present invention describes an immunoglobulin (Ig) light chain
XX binding protein (PI) which has been modified by one or more amino acid
XX substitutions such that the dissociation constant (Kd) of the protein
XX with respect to human Ig kappa-chain is 400 nM or more at pH8. PI is
XX useful in immunofaffinity chromatography. The present sequence encodes a
XX Peptostreptococcus protein L Ig light chain binding domain, which is
XX given in the disclosure of the present invention.
XX
XX Sequence 222 BP; 105 A; 35 C; 40 G; 42 T; 0 other:
SQ

Query Match 82.1%; Score 204.4; DB 21; Length 222;
Best Local Similarity 95.0%; Pred. No. 2.3e-35;
Matches 211; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 22 aaagaaacaccagaacacccagaagaacccaagaagaagttacaatcaatgaactta 81
DB 1 aaagaaacaccagaacacccagaagaacccaagaagaagttacaatcaatgaactta 60
OY 82 atcttcagatggaagatacaaacagcagaattccaagaacatttgaagaagcaaca 141
DB 61 atcttcagatggaagatacaaacagcagaattccaagaacatttgaagaagcaaca 120
OY 142 gcaagaacttacaagatgacagacttattagcaaaagtaagtgcaataacagcagac 201
DB 121 gcaagaacttacaagatgacagacttattagcaaaagtaagtgcaataacagcagac 180
OY 202 ttaagaagatggtggaacacataatgaacattaaattgtctgga 243
DB 181 ttaagaagatggtggaacacataatgaacattaaattgtctgga 222
```

```
RESULT 11
AAA08431
```

```
ID AAA08431 standard; DNA: 213 BP.
XX
XX
AC AAA08431;
XX
XX 20-JUL-2000 (first entry)
XX
XX Peptostreptococcus strain 3316 protein L domain C2 DNA sequence.
XX
XX
XX Immunoglobulin light chain binding protein; PpL; protein L;
XX Peptostreptococcus; human immunoglobulin kappa chain;
XX Immunofaffinity chromatography; ds.
XX
XX Peptostreptococcus sp.
XX WO200015803-A1.
XX
XX 23-MAR-2000.
XX
XX 14-SEP-1999; 99WO-GB03048.
XX
XX 14-SEP-1998; 98GB-0019998.
XX 26-APR-1999; 99GB-0009578.
XX
XX (ACTI-) ACTINOVA LTD.
XX
XX Gore MG, Beckingham JA, Roberts SE;
XX WPI: 2000-271441/23.
XX P-PSDB; AAY82542.
XX
XX New modified immunoglobulin light chain binding protein, useful in
XX immunofaffinity chromatography, has a dissociation constant of 400 nM or
XX more at pH8 with respect to human immunoglobulin kappa-chain -
XX
XX Disclosure; Page 46-47; 56pp; English.
XX
XX The present invention describes an immunoglobulin (Ig) light chain
XX binding protein (PI) which has been modified by one or more amino acid
XX substitutions such that the dissociation constant (Kd) of the protein
XX with respect to human Ig kappa-chain is 400 nM or more at pH8. PI is
XX useful in immunofaffinity chromatography. The present sequence encodes a
XX Peptostreptococcus protein L Ig light chain binding domain, which is
XX given in the disclosure of the present invention.
XX
XX Sequence 213 BP; 100 A; 32 C; 40 G; 41 T; 0 other:
SQ

Query Match 77.0%; Score 191.8; DB 21; Length 213;
Best Local Similarity 94.3%; Pred. No. 1.2e-32;
Matches 199; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 33 agaaacaccagaagaacccaagaagaagttacaatcaatgaacttaacttgcaga 92
DB 3 agaaacaccagaagaacccaagaagaagttacaatcaatgaacttaacttgcaga 62
OY 93 tggaaagatataaacaagacgaattccaagaacatttgaagaagaacagaagctta 152
DB 63 tggaaagacacaacaagacgaattccaagaacatttgaagaagaacagaagctta 122
OY 153 cagatatacgaacttattatgcaaaagttaaattggcgaatatatcagcagacttagaagatg 212
DB 123 tgcattatgcagactattattgcaaaagaatggcgaatatatcagcagacttagaagatg 182
OY 213 tggaaacacatattgaacattaaattgtctgga 243
DB 183 tggaaacacatattgaacattaaattgtctgga 213
```

```
RESULT 12
AAO50452
ID AAO50452 standard; DNA: 921 BP.
XX
XX
AC AAO50452;
```

XX 16-MAY-1994 (first entry)
DT
XX
DE Sequence encoding immunoglobulin light chain binding protein.
XX
XX Immunoglobulin; light chain; binding; identification; purification;
KW separation; ss.
XX
OS E. coli LE392/pHDL, DSM 7054.
XX
PN WO9322342-A.
XX
PD 11-NOV-1993.
XX
PE 28-APR-1993; 93WO-SE00375.
XX
PR 28-APR-1992; 92SE-0001331.
XX
PA (HIGH-) HIGHTECH RECEPTOR AB.
XX
PI Bjoerck L, Sjoerding U;
XX
DR WPI: 1993-368722/46.
XX
DR P-PSDB; AAR42993.
XX
PT New protein L binding light chains of all immunoglobulin classes
PT - for binding purifying and identifying immunoglobulin, also
PT related DNA, vectors and host cells
PS
PS Claim 2; Page 37; 71pp; English.
XX
XX The protein encoded by the sequence (Protein L) is capable of
CC binding to immunoglobulin G light chains. It is useful for binding,
CC separating (purifying) and identifying immunoglobulin and for
CC removing immunoglobulin molecules from serum. Hybrid proteins of the
CC L protein can bind all human immunoglobulin classes and many
CC immunoglobulins from other species. They are highly soluble and
CC retain their binding activity at high temperatures over a pH range
CC of 3-10. They can be immobilised without loss of activity.
XX
SQ Sequence 921 BP; 435 A; 128 C; 172 G; 186 T; 0 other;

Query Match 72.8%; Score 181.2; DB 14; Length 921;
Best Local Similarity 86.3%; Pred. No. 2.6e-30;
Matches 214; Conservative 0; Mismatches 28; Indels 6; Gaps 1;
QY 2 tgaacattaaattgctggaagaacacccagaacacccagaagaacacacgaagaag 61
DB 653 taataattaattgctggaagaacacccagaagaacacccagaagaacacacgaagaag 706
QY 62 ttacaataaattgctggaagaacacccagaagaacacccagaagaacacacgaagaag 121
DB 707 ttacaataaattgctggaagaacacccagaagaacacccagaagaacacacgaagaag 766
QY 122 gaacattgaagaagaacacacgaagaacacacgaagaacacacgaagaacacacgaagaag 181
DB 767 gaacattgaagaagaacacacgaagaacacacgaagaacacacgaagaacacacgaagaag 826
QY 182 atggcgaatatacagcagactagaagaatggaagaacacacgaagaacacacgaagaag 241
DB 827 atggcgaatatacagcagactagaagaatggaagaacacacgaagaacacacgaagaag 886
QY 242 gaacataa 249
DB 887 gtaagaaa 894

RESULT 13
AAC84644
ID AAC84644 standard; DNA; 1305 BP.
XX
AC AAC84644;

XX 20-APR-2001 (first entry)
DT
XX
DE ProL-CBDCex encoding DNA.
XX
XX Recombinant; fusion protein; cellulose binding peptide; CBP; cellulose;
KW food industry; alcoholic beverage; hydrolysis; whey lactose; aspartame;
KW artificial sweetener; milk; animal feed enzyme; heparin; heparan sulfate;
KW protein fiber; effluent treatment; detergent; leather; cell signal; ds.
XX
OS Unidentified.
XX
PN WO20007175-A1.
XX
PD 21-DEC-2000.
XX
PE 17-MAY-2000; 2000WO-US13434.
XX
PR 10-JUN-1999; 99US-0329234.
XX
PA (CBDT-) CBD TECHNOLOGIES LTD.
PA (YISS) YISSUM RES & DEV CO.
PA (FRIE/) FRIEDMAN M M.
XX
PI Shani Z, Shoseyov O;
XX
DR WPI: 2001-080683/09.
XX
PT Expressing and isolating recombinant protein from plant e.g for use in
PT food industry. Involves homogenizing a plant expressing fusion protein
PT including recombinant protein and cellulose binding peptide being fused
PT to it
XX
PS Example 1; Page 58-59; 64pp; English.
XX
XX The invention relates to a process of expressing a recombinant protein in
CC a plant and isolating the recombinant protein from the plant. The method
CC comprises: (a) providing a plant, a plant derived tissue or cultured
CC plant cells expressing a fusion protein (FP) including a recombinant
CC protein and a cellulose binding peptide (CBP) being fused to it; FP
CC being compartmentalized so as to be sequestered from the cell walls;
CC (b) homogenizing the plant, plant derived tissue or cultured plant cells
CC such that FP is brought into contact with a plant derived cellulosic
CC matter (CM) to effect affinity binding of FP via CBP to CM and forming a
CC FP-CM complex; and (c) isolating the FP-CM complex. The recombinant
CC protein isolated by this method is useful commercially in the food
CC industry, for the hydrolysis of high molecular weight protein, in the
CC manufacture of alcoholic beverages, for the hydrolysis of whey lactose,
CC in the production of the artificial sweetener aspartame, in the reduction
CC of the cooked flavour of milk, in the production of animal feed enzymes,
CC in the sterilization and oxidation of plastics and rubbers, for the
CC production of heparin and heparan sulfate oligosaccharides, for
CC purification in industrial processes, for production of protein fibers,
CC for effluent treatment, in combination with detergents in cleaning
CC applications, and in leather manufacturing processes. The present
CC sequence represents a DNA encoding a ProL-CBDCex peptide, used for the
CC construction of CBD-protein-L constructs for expression in transgenic
CC potato tubers.
XX
SQ Sequence 1305 BP; 495 A; 282 C; 293 G; 235 T; 0 other;

Query Match 72.8%; Score 181.2; DB 22; Length 1305;
Best Local Similarity 86.3%; Pred. No. 2.7e-30;
Matches 214; Conservative 0; Mismatches 28; Indels 6; Gaps 1;
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DB 664 taataattaattgctggaagaacacccagaagaacacccagaagaacacacgaagaag 717
QY 62 ttacaataaattgctggaagaacacccagaagaacacccagaagaacacacgaagaag 121
DB 718 ttacaataaattgctggaagaacacccagaagaacacccagaagaacacacgaagaag 777

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 16:35:23 ; Search time 1834.72 Seconds
(without alignments)
2840.056 Million cell updates/sec

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Perfect score: 249
Sequence: 1 atgaacataaattgctgctg.....ttaattgctggaataaa 249

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Maximum Match 0%

Listing first 45 summaries

Database: GenEmbl:
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2: gb_htg:*
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30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_inv:

Pred.-No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Query Score Match Length DB ID Description

1	231.4	92.9	876	6	AR137037	AR137037 Sequence
2	230.4	92.5	876	6	A75725	A75725 Sequence 3
3	229.8	92.3	3258	1	PEPRORF1N	L04466 ReproStrept
4	229.8	92.3	3279	6	A75723	A75723 Sequence 1
5	229.8	92.3	3279	6	A75727	A75727 Sequence 1
6	229.8	92.3	3279	6	AR137036	AR137036 Sequence
7	181.2	72.8	921	6	AR079000	AR079000 Sequence
8	181.2	72.8	1308	6	AR079001	AR079001 Sequence
9	181.2	72.8	1365	1	S50809	S50809 protein IgG
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11	109.8	44.1	548	6	AX022441	AX022441 Sequence
12	109.8	44.1	548	6	AX030798	AX030798 Sequence
13	109.8	44.1	548	6	AX034619	AX034619 Sequence
14	107	43.0	539	6	AX022452	AX022452 Sequence
15	107	43.0	539	6	AX030809	AX030809 Sequence
16	107	43.0	539	6	AX034628	AX034628 Sequence
17	107	43.0	539	6	AX022447	AX022447 Sequence
18	107	43.0	599	6	AX030804	AX030804 Sequence
19	107	43.0	599	6	AX034625	AX034625 Sequence
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21	107	43.0	1031	6	AX030802	AX030802 Sequence
22	107	43.0	1031	6	AX034623	AX034623 Sequence
23	107	43.0	1479	6	AX034630	AX034630 Sequence
24	107	43.0	1490	6	AX022443	AX022443 Sequence
25	107	43.0	1490	6	AX030800	AX030800 Sequence
26	107	43.0	1490	6	AX034621	AX034621 Sequence
27	86.2	34.6	6094	6	AX027906	AX027906 Sequence
28	86.2	34.6	6094	12	AX027912	AX027912 Sequence
29	65.8	26.4	167227	9	AC020602	AC020602 Homo sapi
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ALIGNMENTS

RESULT 1
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LOCUS AR137037 876 bp DNA
DEFINITION Sequence 3 from patent US 6162903.
ACCESSION AR137037
VERSION AR137037.1 GI:14478287
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 876)
AUTHORS Trowern,A.R., Atkinson,A., Murphy,J.P., Laurence,O.S. and Dugdaley,C.J.
TITLE Immunoglobulin binding proteins derived from L protein and their uses
JOURNAL Patent: US 6162903-A 3 19-DEC-2000;
FEATURES
source location/Qualifiers
1..876 /organism="unknown"

BASE COUNT 402 a 141 c 162 g 171 t
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Db	628	ATCAACATTAAATTTGCTGGAAAGAAACACCAAGAAACCCAGAAAGAACCAAAAGAA	687
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QY	121	ggacaatttgaagaagcaacagcagaagcttaacagataltgcagacttaattgaca	180
Db	748	GGAAACATTGGAAGAAAGCAACACGACAGACTTTCAGATTATGCGACGCTTTAT	807
QY	181	aatggcgaatatagacagcagacttagaagaatgttgaaacacatgaacattaattgt	240
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QY	241	ggaaaataa	249
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[illegible]

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Db	808	AATGGTGAATACACAGCAGACTTGAAGATGGCGGATACACTATCAACATCAAAATTGGCT	867
Qy	241	ggaaaata 248	
Db	868	GGAAATA 875	

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LOCUS	3258 bp DNA linear BCT 26-MAY-1991
DEFINITION	Peptostreptococcus magnus protein L gene, complete cds.
ACCESSION	U04466
VERSION	U04466.1 GI:150673
KEYWORDS	protein L, Peptostreptococcus magnus (strain 3316) DNA, Finegoldia magna
SOURCE	Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae; Finegoldia.
ORGANISM	1 (bases 1 to 3258)
REFERENCE	Murphy, J.P., Trowen, A.R. and Duggieby, C.J. Nucleotide sequence of the gene for peptostreptococcal protein L DNA Seq. 4 (4), 255-265 (1994)
FEATURES	95078460 Location/Qualifiers
SOURCE	1. 3258

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Db 1636	GTTACAAATCAAAAGTTAACTTAATCTTTGCAGATGAAAAACCAAAACGAGAAATTCAA 1695			
QY 121	ggacattttggaagaagcaacacgcagaagcttaacagatatgcagacttatgtgcaaaagta 180			
Db 1696	GGAAATTTTGAAGAAGCAACAGCAGAAACCTTACCAATATGACAGACTTTATTACCAAAAGTA 1755			
QY 181	aatggcgaatatacagcagacttagaagatgltggaaccatatagaacatnaatttgc 240			
Db 1756	AATGTTGAATACACACGACAGACTTAGAAGATGGCGGATACACTATCATCAATCAATTGGCT 1815			
QY 241	ggaaataata 249			
Db 1816	GGAAAGAA 1824			
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LOCUS	A75723	3279 bp	DNA	linear
DEFINITION	Sequence 1 from Patent WO9322439.			
ACCESSION	A75723			
VERSION	A75723.1			
KEYWORDS	GI:6065694			
SOURCE	Peptostreptococcus sp. 1018.			
ORGANISM	Peptostreptococcus sp. 1018			
REFERENCE	Bacteria; Filicutes; Bacillus/Clostridium group; Clostridiaceae;			
AUTHORS	Peptostreptococcus.			
TITLE	1 (bases 1 to 3279)			
	Towern, A.R. and Atkinson, A.			
	IMMUNOGLOBULIN BINDING PROTEINS DERIVED FROM L PROTEIN AND THEIR			

JOURNAL Patent: WO 9322439-A 11-NOV-1993;
 HEALTH LAB SERVICE BOARD (GB); TROWERN ANGUS ROBERT (GB)
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 Best Local Similarity 95.2%; Pred. No. 5.2e-33;
 Matches 237; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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 Db 1576 ATCAACATTAAATTTGCGGAAAGAAACACACAGAAACACAGAAACCAAAAGAA 1635
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	ACCESSION	AR079001	
	VERSION	AR079001.1	
	KEYWORDS	GI:10005747	
	SOURCE	Unknown.	
	ORGANISM	Unknown.	
	REFERENCE	Unclassified.	
	AUTHORS	1 (bases 1 to 1308)	
	TITLE	Bjorck,L. and Sjobring,U. Protein L and hybrid proteins thereof Patent: US 5965390-A 4 12-OCT-1999;	
	JOURNAL	Location/Qualifiers	
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Db	707	TTACTATTAAAGCAACACTTAATCTATGACAGATGAGAAAAAATCTAACACAGCAGAGTTCCAAG	766	
QY	122	gaacctttggaagaagacacacagcagaagccttaagatatgacagacttatagcaaaaagtaa	181	
Db	767	GAAACATTTTGCAGAACCAACAGCGAAGCAATACAGATACCTGACTTATTATGCAAAAAAGAA	826	
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[illegible]

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ORGANISM	unclassified.
REFERENCE	1 (bases 1 to 548)
AUTHORS	Koentgen, F., Suess, G.M., Tarlinton, D.M. and Treutlein, H.R.
TITLE	Precursors of catalytic antibodies
JOURNAL	Patent: EP 0935612-A 1 18-AUG-1999;
FEATURES	AMRAD OPERATIONS PTY LTD (AU)
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Best Local Similarity	68.0%; Pred. No. 5.7e-11;
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Oy	205 gaaagttgtgaaacacatagaaacttaatttltgtgaaataa 249
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RESULT 12	
LOCUS	AX030798 548 bp DNA linear PAT 20-SEP-2000
DEFINITION	Sequence 1 from Patent US6043069.
ACCESSION	AX030798
VERSION	AX030798.1 GI:10278297
KEYWORDS	unidentified.
SOURCE	unclassified.
ORGANISM	unclassified.
REFERENCE	1 (bases 1 to 548)
AUTHORS	Koentgen, F., Suess, G.M., Tarlinton, D.M. and Treutlein, H.R.
TITLE	Catalytic antibodies and a method of producing same
JOURNAL	Patent: US 6043069-A 1 28-MAR-2000;
FEATURES	AMRAD OPERATIONS PTY LTD (AU)
source	Location/Qualifiers
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07	85	tttcagatgtgaagaatcaacaacagcagaatccaaggaacatttgaagaagaacagca 144		
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07	145	gaagcttcagatgtgagagactatttagcaaaagtaagttgcgaataatagcagacta 204		
Db	172	GAAAGCTTATGCGCTATGCGATACTTTGAAAGAAAGCAATGGTGAATATCTGTGATGTT 231		
07	205	gaagatgtgtgaaacacataatgaacataaattgtcgtgaaataa 249		
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AX034619	AX034619	548 bp	DNA	Linear
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ACCESSION	AX034619			
VERSION	AX034619.1	GI:10303209		
KEYWORDS				
SOURCE	Flnegoldia magna.			
ORGANISM	Flnegoldia magna			
REFERENCE	Bacteria: Firmicutes; Bacillus/Clostridium group; Clostridiaceae; Flnegoldia.			
AUTHORS	1 (bases 1 to 548)			
TITLE	Koentgen, F., Suess, G.M., Tarlington, D.M. and Treutlein, H.R.			
JOURNAL	Catalytic antibodies and a method of producing same			
	Patent: WO 9915563-A 1 01-APR-1999;			
	KOENTGEN FRANK (AU) ; AMRAD OPERATIONS PTY LTD (AU) ; SUESS			
	HERBERT MARIA (AU) ; TARLINGTON DAVID MATTHEW (AU) ; TREUTLEIN			
	HERBERT RUDOLF (AU)			
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Db	112	TTTGCMAATGTGTAGACACAAACTGCACAATTCAAAGGTACTCTCGAAAAGCGACCTCG 171		
07	145	gaagcttcagatgtgagagactatttagcaaaagtaagttgcgaataatagcagacta 204		
Db	172	GAAAGCTTATGCGCTATGCGATACTTTGAAAGAAAGCAATGGTGAATATCTGTGATGTT 231		
07	205	gaagatgtgtgaaacacataatgaacataaattgtcgtgaaataa 249		
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KEYWORDS				
SOURCE	Flnegoldia magna.			
ORGANISM	Flnegoldia magna			
REFERENCE	Bacteria: Firmicutes; Bacillus/Clostridium group; Clostridiaceae; Flnegoldia.			
AUTHORS	1 (bases 1 to 548)			
TITLE	Koentgen, F., Suess, G.M., Tarlington, D.M. and Treutlein, H.R.			
JOURNAL	Catalytic antibodies and a method of producing same			
	Patent: WO 9915563-A 1 01-APR-1999;			
	KOENTGEN FRANK (AU) ; AMRAD OPERATIONS PTY LTD (AU) ; SUESS			
	HERBERT MARIA (AU) ; TARLINGTON DAVID MATTHEW (AU) ; TREUTLEIN			
	HERBERT RUDOLF (AU)			
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ACCESSION	AX022452		
VERSION	AX022452.1	GI:10046066	
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ORGANISM			
REFERENCE			
AUTHORS	Koentgen,F., Suess,G.M., Tarlinton,D.M. and Treutlein,H.R.		
TITLE	Precursors of catalytic antibodies		
JOURNAL	Patent: EP 0935612-A 12 18-AUG-1999;		
FEATURES	AMRD OPERATIONS Pty Ltd (AU)		
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Oy	115	tccaagaacaactttaagaagaacaagaagaagcttacagatatagcaacttatagca	174
Dd	94	TTCAAAGGTCCTTCGAAAAGGACGACCTCGAAGCTTAGCCGATATGCAGATACTCTTTGAAG	153
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ACCESSION	AX030809		
VERSION	AX030809.1	GI:10278307	
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REFERENCE 1 (bases 1 to 539)
AUTHORS Koentgen, F., Suesse, G.M., Tarlinton, D.M. and Treutlein, H.R.
TITLE Catalytic antibodies and a method of producing same
JOURNAL Patent: US 6043069-A 12 28 -MR-2000;
AMRAD OPERATIONS PTY LTD (AU)
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QY 115 ttcaagggacatttgaagaagcaacagcagaagcttacagatatgcagactattagca 174
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